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	10	20	30	40	50	
NOV_HU	MQSVQSTSFCLRKQCLCLTFLLHLLGQVAAT-----					32
CTGF_H	MTAASMGPRVAVFVLLALCSRPAVG-----					26
zctgf2M	-----					0
zctgf4H	MQGLLFPTLLLAGLAQFCCRVOG-----TGPLDTPPEGRP					35
IBP1_H	MSEVPVARVWLVLVLLTVQVGVTAG-----					25
IBP2_H	MLPRVGCPALPLPPPPLPLPLLLLLLGASG-GGGGARAELFRCPCT					49
	60	70	80	90	100	
NOV_HU	-----QRCPPQCPGRCPATP-PTCAPGVRAVLGDCSCCLVCARQR					71
CTGF_H	-----QNC\$GPCR--CPDEPAPRCAGVSLVLDGCGCCRVCAKQL					64
zctgf2M	-----					0
zctgf4H	GEVSDAPQRKQFCHWPCK--CPQK-PRCPPGVSLVRDGCCKICAKQP					82
IBP1_H	---APWQCAPCSAEKLAL--CPPVS-ASCSEVTR--SAGCGCCPMCALPL					67
IBP2_H	PERLAACGPPPAPPAAVAAVAGGARMPCAELVR--EPGCGCCSVCARLE					97
	110	120	130	140	150	
NOV_HU	GESCSLEPCDESSGLYCDRSADPSN-QTGICTAVEGD-NCVFDGVIYRS					119
CTGF_H	GELCTERDPCDPHKGLFCDFGSPANR-KIGVCTAKDGA-PCIFGGTVYRS					112
zctgf2M	-----					0
zctgf4H	GEICNEADLCDPHKGLYCDYSVDRPRYETGVCAYLAV-GCEFNQVHYHN					131
IBP1_H	GAACGVATARCARGLSR-----					85
IBP2_H	GEACGVYTPRCGQGLRCY-----					115
	160	170	180	190	200	
NOV_HU	GEKFQPSCKFQCTCRDGGQIGCVPRCQLDVLLPEPNCAPARKVEVPGECC					169
CTGF_H	GESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFPRRVKLPKGCCE					162
zctgf2M	-----					0
zctgf4H	GQVFQPNPLFSCLCVSGAIGCTPL--FIPKLAGSHCSGAK---GGKKSD					175
IBP1_H	-----					85
IBP2_H	-----					115
	210	220	230	240	250	
NOV_HU	KWICGPDEEDSLGGL---TLAAYRPEATLGVEVSDSSVNCIEQTTEWTAC					216
CTGF_H	EWVC--DEPK-DQTVVGPALAAYRLEDTFGPDPTMIRANCLVQTTEWSAC					209
zctgf2M	-----NVVYLPAYRNLPLIWKKKCLVQATKWTPC					29
zctgf4H	QSN--SLEP---LLQQLSTS YKTPAYRNLPLIWKKKCLVQATKWTPC					219
IBP1_H	-----					85
IBP2_H	-----					115

Fig. 1A

	260	270	280	290	300	
NOV_HU	SKSCGMGFSTRVTNRNRQCEMLKQTRL	CMVRPCEQEPEQ-PTDKKGKKCL				265
CTGF_H	SKTCGMGISTRVTNDNASCRLEKQSR	LCMVRPCEADLE--ENIKKGKKCI				257
ZCTGF2M	S-----				IPRGETCQ	38
zctgf4H	SRTCGMGISNRVTNENSNC	EMRKEKRLCYIQPCDSN	ILKTIKIPKGKTCQ			269
IBP1_H	-----					85
IBP2_H	-----					115

	310	320	330	340	350	
NOV_HU	RT-KKSLKAIHLQFKNCTSLHTYKPR	FCGVCS	DGR	CCTPHNTKTIQAEFQ		314
CTGF_H	RTPKISKPIKFE-LSGCTSMKTYRAK	FCGVCTDGR	CCTPHRTTTL	PVEFK		306
ZCTGF2M	PTFQLPKAEKFV-FSGCSSTQSYRPT	FCGICLDRCCVPNKS	KMITVRFD			87
zctgf4H	PTFQLSKAEKFV-FSGCSSTQSYKPT	FCGICLDRCCIPNKS	KMITIQFD			318
IBP1_H	-----					85
IBP2_H	-----					115

	360	370	380	390	
NOV_HU	CSPGQIVKKPVMVIGTCTCHTNCPKN	NEAFLQELKTTTRGK--			356
CTGF_H	CPDGEVMKKNMFIKTCACHYNCPGD	NDIFESLYRKMYGDM--			348
ZCTGF2M	CPSEGSFKWQMLWVTSCVCQRDCRE	PGDIFSELRL-----			123
zctgf4H	CPNEGSFKWKMLWITSCVCQRNCRE	PGDIFSELKIL-----			354
IBP1_H	-----				85
IBP2_H	-----				115

Fig. 1B